

- 1 -
piece 1, NC_000913, yjbM_dusA-, config: linear, direction: -, begin: 4259766, end: 4259310



- 2 -

The figure shows a sequence logo for the p35-p10 4259501 construct. The top part displays the total sequence with various mutations marked by red dots and labeled with IDs like *4259440, *4259430, etc. Below the sequence, the amino acid sequence is shown with mutations indicated by red dots above the letters. The bottom part is divided into three regions: p35 (1.6 bits), p10 (5.3 bits), p10 (2.5 bits), and p10 (2.7 bits). Each region has its own sequence logo. A gap between the first and second p10 region is labeled as 2.3 bits.

|-----| p35-p10_4259411 total 4.5 bits

p35 5, 6 bits

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{p35-(24)-p10 4259382 Gap 2.4 bits  
p35-p10 4259382 total 5.7 bits  
}p35-(25)-p10 4259381 Gap 4.0 bits  
p35-p10 4259381 total 4.3 bits
```

|-----| p33-p34 4235531 total 4.3 Bits

*4259350 *4259340 *4259330 *4259320 *4259310

5' *4259360 *4259350 *4259340 *4259330 *4259320 *4259310
 -fMet - pro - ile - leu - ser - lys - asn - phe - thr - tyr - tyr - phe - ser - asp - leu - thr -
 -
 - ala - phe - his - thr - ile - glu - glu - leu - his - ile - leu - phe - leu - arg - phe - asn -

... NC_000913.yjbM